VERSION WITH MARKINGS TO SHOW CHANGES MADE

Changes to the Specification

On page 11, lines 9-19 the following paragraph was substituted for the original paragraph.

In a preferred embodiment, differentially expressed sequences are those that are up-regulated in breast cancer and/or colorectal cancer; that is, the expression of these genes is higher in carcinoma as compared to normal breast or colon tissue. "Up-regulation as used herein means at least about a 50% increase, preferably a two-fold change, more preferably at least about a three fold change, with at least about five-fold or higher being preferred. All accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see e.g., Benson, DA et al., Nucleic Acids Research 26:1-7 (1998) [and http://www.ncbi.nlm.nih.gov/]. In addition, these genes were found to be expressed in a limited amount or not at all in heart, brain, lung, liver, kidney, muscle, pancreas, testes, stomach, small intestine and spleen.

On page 15 of the specification, lines 17-30 the following paragraph was substituted for the original paragraph.

Another example of a useful algorithm is the BLAST algorithm, described in Atschul et al., J. Mol. Biol. 215, 403-410 (1990) and Karlin et al., PNAS USA 90:5873-5787 (1993). A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Atschul et al., Methods in Enzymology, 266:460-480 (1996) [[http://blast.wustl/edu/blast/READ.html]]. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span =1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and the

composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided by the total number of residues of the "longer" sequence in the aligned region. The "longer" sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-BLAST-2 to maximize the alignment score are ignored).

Changes to the Claims

32. (Amended) A method of diagnosing breast cancer or colorectal cancer comprising:

a) determining the expression of a [gene] nucleic acid [at least 75% identical to] that encodes an amino acid sequence at least 95% identical to SEQ ID NO:2. in a first sample of a first individual; and

[(]b) comparing the expression of said [gene(s)] nucleic acid in the first sample to expression of said [gene] nucleic acid in a second sample; [wherein said comparison is used to diagnose] wherein an increase in expression of said nucleic acid in the first sample relative to the second sample provides a diagnosis of breast cancer or colorectal cancer in the first individual.

34. (Amended) The method of claim 33, wherein said first sample is[breast tissue or] colorectal tissue.

35. (Amended) The method of claim 33, wherein said second sample is [breast tissue or] colorectal tissue.

38. (Amended) The method of claim 37, wherein said first sample is [breast tissue or] colorectal tissue.

39. (Amended) The method of claim 37, wherein said second sample is [breast tissue or] colorectal tissue.

41. (Amended) The method of claim 32, wherein said [gene is] nucleic acid comprises SEQ ID NO:1.

44. (Amended) A method for determining the prognosis of an individual with breast cancer or colorectal cancer comprising determining the expression of a [gene] nucleic acid [at least 75% identical to] that encodes an amino acid sequence at least 95% identical to SEQ ID NO:2 in a sample from an individual, wherein a high level of expression of said sequence indicates a poor [the expression of the gene is used to determine the] prognosis [of] for the individual.

45. (Amended) The method of claim 44, wherein said [gene is] nucleic acid comprises SEQ ID NO:1.

APPENDIX A: CLAIMS CURRENTLY PENDING IN THIS APPLICATION

32. (Amended) A method of diagnosing breast cancer or colorectal cancer comprising:

a) determining the expression of a nucleic acid that encodes an amino acid sequence at least 95% identical to SEQ ID NO:2. in a first sample of a first individual; and

b) comparing the expression of said nucleic acid in the first sample to expression of said nucleic acid in a second sample; wherein an increase in expression of said nucleic acid in the first sample relative to the second sample provides a diagnosis of breast cancer or colorectal cancer in the first individual.

33. The method of claim 32, wherein said second sample is from said first individual.

34. (Amended) The method of claim 33, wherein said first sample is colorectal tissue.

35. (Amended) The method of claim 33, wherein said second sample colorectal tissue.

36. (Cancelled)

37. The method of claim 32, wherein said second sample is from a second individual.

38. (Amended) The method of claim 37, wherein said first sample is colorectal tissue.

39. (Amended) The method of claim 37, wherein said second sample is colorectal tissue.

40. (Cancelled)

41. (Amended) The method of claim 32, wherein said nucleic acid comprises SEQ ID NO:1.

42. The method of claim 32, wherein said expression is measured using a labeled nucleic acid probe.

43. The method of claim 32, wherein said expression is measured utilizing a biochip.

44. (Amended) A method for determining the prognosis of an individual with breast cancer or colorectal cancer comprising determining the expression of a nucleic acid that encodes an amino acid sequence at least 95% identical to SEQ ID NO:2 in a sample from an individual, wherein a high level of expression of said sequence indicates a poor prognosis for the individual.

45. (Amended) The method of claim 44, wherein said nucleic acid comprises SEQ ID NO:1.

46. The method of claim 44, wherein said expression is measured using a labeled nucleic acid probe.

47. The method of claim 44, wherein said expression is measured utilizing a biochip.

48. The method of claim 33, wherein said first sample is breast tissue.

49. The method of claim 33, wherein said second sample is breast tissue.

50. (Amended) The method of claim 37, wherein said first sample is breast tissue.

51. (Amended) The method of claim 37, wherein said second sample is breast tissue.